Amendments to the Claims under Revised 37 C.F.R. § 1.121

Claim 1 (currently amended): A truncated sTNFR polypeptide comprising:

~~(a)~~ amino acid residues 1-110, 1-109, 1-108, 1-107, 1-106, 1-105, 1-104, 1-103, 2-110, 2-109, 2-108, 2-107, 2-106, 2-105, 2-104, 2-103, 3-110, 3-109, 3-108, 3-107, 3-106, 3-105, 3-104, 3-103, 4-110, 4-109, 4-108, 4-107, 4-106, 4-105, 4-104, 4-103, 5-110, 5-109, 5-108, 5-107, 5-106, 5-105, 5-104, 5-103, 6-110, 6-109, 6-108, 6-107, 6-106, 6-105, 6-104, 6-103, 7-110, 7-109, 7-108, 7-107, 7-106, 7-105, 7-104, 7-103, 8-110, 8-109, 8-108, 8-107, 8-106, 8-105, 8-104, 8-103, 9-110, 9-109, 9-108, 9-107, 9-106, 9-105, 9-104, 9-103, 10-110, 10-109, 10-108, 10-107, 10-106, 10-105, 10-104, 10-103, 11-110, 11-109, 11-108, 11-107, 11-106, 11-105, 11-104, 11-103, 12-110, 12-109, 12-108, 12-107, 12-106, 12-105, 12-104, 12-103, 13-110, 13-109, 13-108, 13-107, 13-106, 13-105, 13-104, 13-103, 14-110, 14-109, 14-108, 14-107, 14-106, 14-105, 14-104, 14-103, 15-110, 15-109, 15-108, 15-107, 15-106, 15-105, 15-104, 15-103, 16-110, 16-109, 16-108, 16-107, 16-106, 16-105, 16-104, 16-103, 17-110, 17-109, 17-108, 17-107, 17-106, 17-105, 17-104, 17-103, 18-110, 18-109, 18-108, 18-107, 18-106, 18-105, 18-104, 18-103, 19-110, 19-109, 19-108, 19-107, 19-106, 19-105, 19-104, or 19-103 of SEQ ID NO: 2;

provided however, that when the truncated sTNFR polypeptide comprises amino acid residues 1-110, 2-110, 3-110, 4-110, 5-110, 6-110, 7-110, 8-110, 9-110, 10-110, 11-110, 12-110, 13-110, 14-110, 15-110, 16-110, 17-110, 18-110, or 19-110 of SEQ ID NO: 2, the polypeptide does not further comprise amino acid residues 111-161 of SEQ ID NO: 2, or a portion thereof;

~~(b) the amino acid sequence of (a) with at least one amino acid substitution;~~

~~(c) the amino acid sequence of (a) with at least one amino acid addition; or~~

~~(d) the amino acid sequence of (a) with at least one internal intrasequence amino acid deletion;~~

and optionally further comprising an amino-terminal methionine.

Claim 2 (currently amended): An isolated truncated sTNFR polypeptide comprising:

~~(a)~~ the amino acid sequence as set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 12, SEQ ID NO: 10, or SEQ ID NO: 14;

~~(b) the amino acid sequence of (a) with at least one amino acid substitution;~~

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~~(c) the amino acid sequence of (a) with at least one amino acid addition, provided that the polypeptide does not comprise amino acid residues 111-161 of SEQ ID NO: 2 or a portion thereof; or~~

~~(d) the amino acid sequence of (a) with at least one internal intrasequence amino acid deletion.~~

Claim 3 (cancelled).

Claim 4 (previously presented): The polypeptide of either Claim 1 or 2, wherein said amino acid sequence is nonglycosylated.

Claim 5 (previously presented): The polypeptide of either Claim 1 or 2, wherein said amino acid sequence is glycosylated.

Claim 6 (previously presented): The polypeptide of either Claim 1 or 2, wherein the protein is conjugated to a water soluble polymer.

Claim 7 (previously presented): A polyvalent truncated sTNFR molecule comprising at least one polypeptide of either Claim 1 or 2.

Claim 8 (previously presented): A polyvalent molecule having the formula R_1-X-R_2, wherein:

X comprises a linker, wherein said linker is a water soluble polymer; and

R_1 and R_2 are biologically-active molecules covalently bonded to said water soluble polymer, wherein at least one of R_1 and R_2 is a polypeptide of either Claim 1 or 2.

Claim 9 (previously presented): The polyvalent molecule of Claim 8, wherein the water soluble polymer is polyethylene glycol.

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Claim ~~10~~ 13 (previously presented): The polyvalent molecule of Claim ~~9~~ 12, wherein R_1 and R_2 are polypeptides comprising:

(a) the amino acid sequence as set forth in SEQ ID NO: 4; or

(b) the amino acid sequence as set forth in SEQ ID NO: 6.

Claim 11-21 (cancelled).

Claim ~~22~~ 14 (previously presented): A truncated sTNFR polypeptide which is the recombinant expression product of a prokaryotic or eukaryotic host cell containing an exogenous polynucleotide encoding the polypeptide of either Claim 1 or 2.

Claim ~~23~~ 15 (previously presented): A pharmaceutical composition comprising the polypeptide of either Claim 1 or 2 in association with a pharmaceutically acceptable vehicle.

Claim ~~24~~ 16 (currently amended): A pharmaceutical composition comprising:

A) a polypeptide produced by a process comprising the steps of growing a prokaryotic or eukaryotic host cell containing a polynucleotide encoding the polypeptide of either Claim 1 or 2 in a suitable nutrient medium and~~, optionally,~~ isolating the polypeptide from the host cell or nutrient medium; and

B) a pharmaceutically acceptable vehicle.

Claim ~~25~~ 17 (currently amended): A pharmaceutical composition comprising:

A) a polypeptide produced by a process comprising the steps of:

(a) culturing a prokaryotic or eukaryotic host cell containing a polynucleotide encoding the polypeptide of either Claim 1 or 2;

(b) maintaining the host cell under conditions allowing the expression of the polypeptide by the host cell; and

(c) ~~optionally~~ isolating the polypeptide expressed by the host cell; and

B) a pharmaceutically acceptable vehicle.

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Claims 26 and 27 (cancelled).

Claim ~~28~~ 18 (previously presented): A method of preparing a pharmaceutical composition wherein a therapeutically effective amount of the polypeptide of either Claim 1 or 2 is mixed with one or more pharmaceutically acceptable vehicles.

Claims 29 and 30 (cancelled).

Claim ~~31~~ 19 (currently amended): A kit for preparing an aqueous protein formulation comprising a first container having the polypeptide of either Claim 1 or 2 and a second container having a physiologically acceptable solvent.

Claim ~~32~~ 20 (previously presented): The polypeptide of either Claim 1 or 2, wherein the protein is fused to a heterologous amino acid sequence.

Claim ~~33~~ 21 (previously presented): The polypeptide of Claim 32, wherein the heterologous amino acid sequence is an IgG constant domain or fragment thereof.

Claim ~~34~~ 22 (currently amended): A truncated sTNFR polypeptide which is the recombinant expression product of a prokaryotic or eukaryotic host cell containing an exogenous polynucleotide comprising a nucleotide sequence:

(a) as set forth in SEQ ID NO: 3;

(b) as set forth in SEQ ID NO: 5;

(c) as set forth in SEQ ID NO: 7;

(d) as set forth in SEQ ID NO: 11;

(e) as set forth in SEQ ID NO: 9;

(f) as set forth in SEQ ID NO: 13;

(g) that is a degenerate ~~in the coding regions or portions thereof~~ sequence of the

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nucleotide sequence of any of (a) - (f); or

(h) ~~that hybridizes to the complement of~~ the nucleotide sequence of any of (a) - (g) encoding a polypeptide that is at least 90 percent identical to the polypeptide encoded by ~~at 45°C in a hybridization buffer comprising 4x SSC and 0.1% SDS~~;

provided however, that the polypeptide does not comprise amino acid residues 111-161 of SEQ ID NO: 2 or a portion thereof;

and optionally further comprising a nucleotide sequence encoding an amino-terminal methionine.

Claim 35 (currently amended): A truncated sTNFR polypeptide which is the recombinant expression product of a prokaryotic or eukaryotic host cell containing an exogenous polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 9, or SEQ ID NO: 13, or a ~~portion~~ TNF inhibitory fragment thereof.

Claim 36 (currently amended): A pharmaceutical composition comprising:

A) a polypeptide produced by a process comprising growing a prokaryotic or eukaryotic host cell containing a polynucleotide comprising a nucleotide sequence:

(a) as set forth in SEQ ID NO: 3;

(b) as set forth in SEQ ID NO: 5;

(c) as set forth in SEQ ID NO: 7;

(d) as set forth in SEQ ID NO: 11;

(e) as set forth in SEQ ID NO: 9;

(f) as set forth in SEQ ID NO: 13;

(g) that is a degenerate ~~in the coding regions or portions thereof~~ sequence of the nucleotide sequence of any of (a) - (f); or

(h) ~~that hybridizes to the complement of~~ the nucleotide sequence of any of (a) - (g) encoding a polypeptide that is at least 90 percent identical to the polypeptide encoded by ~~at 45°C in a hybridization buffer comprising 4x SSC and 0.1% SDS~~;

provided however, that the polypeptide does not comprise amino acid residues 111-161 of SEQ ID NO: 2 or a portion thereof;

and optionally further comprising a nucleotide sequence encoding an amino-

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terminal methionine;

in a suitable nutrient medium and~~, optionally,~~ isolating the polypeptide from the host cell or nutrient medium; and

B) a pharmaceutically acceptable vehicle.

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Claim 37 (currently amended): A pharmaceutical composition comprising:

A) a polypeptide produced by a process comprising growing a prokaryotic or eukaryotic host cell containing a polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 9, or SEQ ID NO: 13, or a ~~portion~~ TNF inhibitory fragment thereof, in a suitable nutrient medium and~~, optionally,~~ isolating the polypeptide from the host cell or nutrient medium; and

wherein the polypeptide does not comprise amino acid residues 111-161 of SEQ ID NO: 2 or a portion thereof

B) a pharmaceutically acceptable vehicle.

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Claim 38 (currently amended): A pharmaceutical composition comprising:

A) a polypeptide produced by a process comprising:

(a) culturing a prokaryotic or eukaryotic host cell containing a polynucleotide comprising a nucleotide sequence:

(i) as set forth in SEQ ID NO: 3;

(ii) as set forth in SEQ ID NO: 5;

(iii) as set forth in SEQ ID NO: 7;

(iv) as set forth in SEQ ID NO: 11;

(v) as set forth in SEQ ID NO: 9;

(vi) as set forth in SEQ ID NO: 13;

(vii) that is a ~~degenerate in the coding regions or portions thereof~~ sequence of the nucleotide sequence of any of (i) - (vi); or

encoding a polypeptide that is at least 90 percent identical to the polypeptide encoded by

(viii) ~~that hybridizes to the complement of~~ the nucleotide sequence of any of (i) - (vii) ~~at 45°C in a hybridization buffer comprising 4x SSC and 0.1% SDS~~;

provided however, that the polypeptide does not comprise amino acid

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residues 111-161 of SEQ ID NO: 2 ~~or~~ or a portion thereof;

and optionally further comprising a nucleotide sequence encoding an amino-terminal methionine;

(b) maintaining the host cell under conditions allowing the expression of the polypeptide by the host cell; and

(c) ~~optionally~~ isolating the polypeptide expressed by the host cell; and

B) a pharmaceutical acceptable vehicle.

Claim ~~39~~ 27 (currently amended): A pharmaceutical composition comprising:

A) a polypeptide produced by a process comprising:

(a) culturing a prokaryotic or eukaryotic host cell containing a polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 9, or SEQ ID NO: 13, or a ~~portion~~ TNF inhibitory fragment thereof, in a suitable nutrient medium; wherein the polypeptide does not comprise amino acid residues 111-161 of SEQ ID NO:2 or a portion there of,

(b) maintaining the host cell under conditions allowing the expression of the polypeptide by the host cell; and

(c) ~~optionally~~ isolating the polypeptide expressed by the host cell; and

B) a pharmaceutical acceptable vehicle.

Claim ~~40~~ 6 (previously presented): The polypeptide of Claim ~~6~~ 5, wherein the water soluble polymer is polyethylene glycol.

Claim ~~41~~ 8 (previously presented): A pharmaceutical composition comprising the polyvalent truncated sTNFR molecule of Claim 7 in association with a pharmaceutically acceptable vehicle.

Claim ~~42~~ 9 (previously presented): A method of preparing a pharmaceutical composition wherein a therapeutically effective amount of the polyvalent truncated sTNFR molecule of Claim 7 is mixed with one or more pharmaceutically acceptable vehicles.

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Claim 43 (currently amended): A kit for preparing an aqueous protein formulation comprising a first container having the polyvalent truncated sTNFR molecule of Claim 7 and a second container having a physiologically acceptable solvent.

Claim 44 (previously presented). The polypeptide of either Claim 1 or 2, wherein the amino acid substitution, amino acid addition, or intrasequence amino acid deletions do not occur in the first two disulfide loops of domain 1, the whole of domain 2, or the first disulfide loop of domain 3 of the polypeptide.

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